(a) a nucleotide sequence encoding a polypeptide having farnesyltransferase activity, wherein the polypeptide has an amino acid sequence of at least 80% sequence identity, based on the Clustal method of alignment, when compared to SEQ ID NO:12, or

(b) a complement of the nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.

33. (new) The polynucleotide of Claim 32, wherein the amino acid sequence of the polypeptide has at least 85% sequence identity, based on the Clustal method of alignment, when compared to SEQ ID NO:12.

34. (new) The polynucleotide of Claim 32, wherein the amino acid sequence of the polypeptide has at least 95% sequence identity, based on the Clustal method of alignment, when compared to SEQ ID NO:12.

35. (new) The polynucleotide of Claim 32, wherein the amino acid sequence of the polypeptide comprises SEQ ID NO:12.

36. (new) The polynucleotide of Claim 32 wherein the nucleotide sequence comprises SEQ ID NO:11.

37. (new) A vector comprising the polynucleotide of Claim 32.

38. (new) A recombinant DNA construct comprising the polynucleotide of Claim 32 operably linked to at least one regulatory sequence.

39. (new) A method for transforming a cell, comprising transforming a cell with the polynucleotide of Claim 32.

40. (new) A cell comprising the recombinant DNA construct of Claim 38.

41. (new) A method for producing a plant comprising transforming a plant cell with the polynucleotide of Claim 32 and regenerating a plant from the transformed plant cell.

42. (new) A plant comprising the recombinant DNA construct of Claim 38.

43. (new) A seed comprising the recombinant DNA construct of Claim 38.

44. (new) An isolated polypeptide having farnesyltransferase activity, wherein the polypeptide has an amino acid sequence of at least 80% sequence identity, based on the Clustal method of alignment, when compared to SEQ ID NO:12.

45. (new) The polypeptide of Claim 44, wherein the amino acid sequence of the polypeptide has at least 85% sequence identity, based on the Clustal method of alignment, when compared to SEQ ID NO:12.

46. (new) The polypeptide of Claim 44, wherein the amino acid sequence of the polypeptide has at least 95% sequence identity, based on the Clustal method of alignment, when compared to SEQ ID NO:12.

47. (new) The polypeptide of Claim 44, wherein the amino acid sequence of the polypeptide comprises SEQ ID NO:12.

48. (new) A method of altering the level of expression of a farnesyltransferase in a host cell comprising:

(a) transforming a host cell with the recombinant DNA construct of Claim 38; and

(b) growing the transformed host cell under conditions that are suitable for expression of the recombinant DNA construct wherein expression of the recombinant DNA construct results in production of altered levels of the farnesyltransferase in the transformed host cell.

Please amend the following claims 15, 21 and 22:

15. (amended) A method of selecting an isolated polynucleotide that affects the level of expression of a farnesyltransferase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least 30 contiguous nucleotides of SEQ ID NO:11, or a complement of such nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of farnesyltransferase polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of farnesyltransferase polypeptide in the plant cell containing the isolated polynucleotide with the level of farnesyltransferase polypeptide in a plant cell that does not contain the polynucleotide.

21. (amended) A method of obtaining a nucleic acid fragment encoding a substantial portion of a farnesyltransferase gene comprising the steps of:

(a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least 40 contiguous nucleotides of SEQ ID NO:11, or a complement of such nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

22. (amended) A method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a farnesyltransferase protein comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least 30 contiguous nucleotides of SEQ ID NO:11, or a complement of such nucleotide sequence, wherein the complement and

the nucleotide sequence consist of the same number of nucleotides and are 100% complementary;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) optionally sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.